

## **WHAT IS CLAIMED IS:**

- 1                   1.     A method of screening drug candidates comprising:
  - 2                   a) providing a cell that expresses an expression profile gene selected from
  - 3                   the group selected of Egr-1, Egr-2, Nur77, c-myc, MIP-1a, MIP-1b, BL34, gfi-1, NAB2,
  - 4                   neurogranin, SLAP, A1, E2-20K, SATB1, Cctq, kappa V, pcp-4, TGIF, CD83, ApoE,
  - 5                   Aeg-2, CD72, cyclin D2, lck, MEF-2C, bmk, IgD, Evi-2, vimentin, CD36, c-fes, c-fos,
  - 6                   TRAP, hIP30, Ly6E.1, LRG-21, Fos B, gadd153, mafK, Ah-R, C/EBP beta, EZF, TIS7,
  - 7                   TIS11, TIS11b, LSIRF, MKP1, PAC-1, PEP, MacMARCKS, SNK, Stra13, kir/gem,
  - 8                   EB12, IL1-R2, MyD116, RP105, uPAR, 4F2, hRab30, Id3, BKLF, LKLF, EFP, bcl-3,
  - 9                   caspase 2, GILZ, hIFI-204, hRhoH, TRAF5, LT-beta, IFNg-RII, gadd45, CDC47, NAG,
  - 10                  scd2, kappa 0 ig, iap38, G7e, B29, and SCD2;
  - 11                  b) adding a drug candidate to the cell; and
  - 12                  c) determining the effect of the drug candidate on the expression of the
  - 13                  expression profile gene.
- 1                   2.     A method according to claim 1 wherein the determining comprises
- 2                   comparing the level of expression in the absence of the drug candidate to the level of
- 3                   expression in the presence of the drug candidate.
- 1                   3.     A method according to claim 1 wherein the cell expresses an
- 2                   expression profile gene set of at least one expression profile gene, and the effect of the
- 3                   drug candidate on the expression of the set is determined.
- 1                   4.     A method according to claim 3 wherein the set comprises a
- 2                   tolerance set comprising carb anH II, IgD, CD72, SATB1, ApoE, CD83, cyclin D2, Cctq,
- 3                   MEF-2C, TGIF, Aeg-2, Egr-1, lck, Egr-2, E2-20K, pcp-4, kappa V, neurogranin, NAB2,
- 4                   gfi-1 hIP-30, TRAP, bmk, CD36, Evi-2, vimetin, Ly6E.1, and c-fes.
- 1                   5.     A method according to claim 4 wherein the expression of hIP-30,
- 2                   TRAP, bmk, CD36, Evi-2, and c-fes are decreased and the expression of carb anH II,
- 3                   CD72, SATB1, ApoE, CD83, cyclin D2, Cctq, MEF-2C, TGIF, Aeg-2, Egr-1, lck, Egr-2,
- 4                   E2-20K, pcp-4, kappa V, neurogranin, NAB2, gfi-1 are increased as a result of the
- 5                   introduction of the drug candidate.

1                   6.     A method according to claim 3 wherein the set comprises a  
2 stimulation set comprising Egr-1, Egr-2, NAB2, mafK, LRG-21, c-fos, c-myc, Stra13,  
3 AhR, gadd153, C/EBP beta, TIS11b, TIS11, gfi-1, EZF, Nur77, LSIRF, SNK, PAC-1,  
4 kir/gem, MacMARCKS, PEP, MKP1, hRab30, MIP-1b, MIP-1a, EB12, BL34, IL1-R2,  
5 TIS7, MyD116, A1, uPAR, RP105, Evi-2 4F2, CD72, Id3, BKLF, LKLF, EFP, Stat1,  
6 bcl-3, hRhoH, TRAF5, SLAP, LT-beta, IFNg-RII, GILZ. Caspase 2, gadd45, CDC47,  
7 NAG, scd2, kappa 0 ig, B29, iap38, G7e, and hIFI-204.

1                   7.     A method according to claim 6 wherein the expression of Id3,  
2 BKLF, LKLF, EFP, Stat1, bcl-3, hRhoH, TRAF5, SLAP, LT-beta, IFNg-RII, GILZ.  
3 Caspase 2, gadd45, CDC47, NAG, scd2, kappa 0 ig, B29, iap38, G7e, and hIFI-204 are  
4 decreased and the expression of Egr-1, Egr-2, NAB2, mafK, LRG-21, c-fos, c-myc,  
5 Stra13, AhR, gadd153, C/EBP beta, TIS11b, TIS11, gfi-1, EZF, Nur77, LSIRF, SNK,  
6 PAC-1, kir/gem, MacMARCKS, PEP, MKP1, hRab30, MIP-1b, MIP-1a, EB12, BL34,  
7 IL1-R2, TIS7, MyD116, A1, uPAR, RP105, Evi-2 4F2, CD72 are increased as a result of  
8 the introduction of the drug candidate.

1                   8.     A method according to claim 3 wherein the set comprises an  
2 immunosuppression set comprising hIFI-204, hRhoH, caspase 2, B29, SLAP, NAG,  
3 iap38, gadd45, BKLF, G7e, Id3, scd2, GILZ, Stat1, kappa 0 ig, LT-beta, LKLF, IFNg-  
4 RII, mCDC47, EFP, TRAF5, and bcl-3.

1                   9.     A method according to claim 8 wherein the expression of hIFI-204,  
2 hRhoH, caspase 2, B29, SLAP, NAG, iap38, gadd45, BKLF, G7e, Id3, scd2, GILZ, Stat1,  
3 kappa 0 ig, LT-beta, LKLF, IFNg-RII, mCDC47, EFP, TRAF5, and bcl-3 are decreased  
4 and the expression of LSIRF, kir/gem, MKP1, hRab30, AhR, c-myc, IL1-R2, TIS11b, Evi-  
5 2, A1, EB12, MyD116, MacMARCKS, MIP-1b, MIP-1a, PEP, CD72 are increased as a  
6 result of the introduction of the drug candidate.

1                   10.    A method according to claim 8 wherein the immunosuppressive set  
2 further comprises c-fos, gadd153, EZF, C/EBP beta, Stra13, NAB2, mafK, and LRG-21.

1                   11.    A method according to claim 10 wherein the expression of c-fos,  
2 gadd153, EZF, C/EBP beta, Stra13, NAB2, mafK, and LRG-21 are increased as a result  
3 of the introduction of the drug candidate.

1 12. A method of screening for a bioactive agent capable of binding to a  
2 B lymphocyte modulator protein (BLMP), the method comprising combining the BLMP  
3 and a candidate bioactive agent, and determining the binding of the candidate agent to the  
4 BLMP.

1 13. A method according to claim 11 wherein the BLMP is selected  
2 from the group consisting of Egr-1, Egr-2, Nur77, c-myc, MIP-1a, MIP-1b, BL34, gfi-1,  
3 NAB2, neurogranin, SLAP, A1, E2-20K, SATB1, Cctq, kappa V, pcp-4, TGIF, CD83,  
4 ApoE, Aeg-2, CD72, cyclin D2, 1ck, MEF-2C, bmk, IgD, Evi-2, vimentin, CD36, c-fes,  
5 c-fos, TRAP, hIP30, Ly6E.1, LRG-21, Fos B, gadd153, mafK, Ah-R, C/EBP beta, EZF,  
6 TIS7, TIS11, TIS11b, LSIRF, MKP1, PAC-1, PEP, MacMARCKS, SNK, Stra13,  
7 kir/gem, EB12, IL1-R2, MyD116, RP105, uPAR, 4F2, hRab30, Id3, BKLf, LKLF, EFP,  
8 bcl-3, caspase 2, GILZ, hIFI-204, hRhoH, TRAF5, LT-beta, IFNg-RII, gadd45, CDC47,  
9 NAG, scd2, kappa 0 ig, iap38, G7e, B29, and SCD2.

1 14. A method for screening for a bioactive agent capable of modulating  
2 the activity of a B lymphocyte modulator protein (BLMP), the method comprising  
3 combining the BLMP and a candidate bioactive agent, and determining the effect of the  
4 candidate agent on the bioactivity of the BLMP.

1 15. A method according to claim 13 wherein the BLMP is selected  
2 from the group consisting of Egr-1, Egr-2, Nur77, c-myc, MIP-1a, MIP-1b, BL34, gfi-1,  
3 NAB2, neurogranin, SLAP, A1, E2-20K, SATB1, Cctq, kappa V, pcp-4, TGIF, CD83,  
4 ApoE, Aeg-2, CD72, cyclin D2, 1ck, MEF-2C, bmk, IgD, Evi-2, vimentin, CD36, c-fes,  
5 c-fos, TRAP, hIP30, Ly6E.1, LRG-21, Fos B, gadd153, mafK, Ah-R, C/EBP beta, EZF,  
6 TIS7, TIS11, TIS11b, LSIRF, MKP1, PAC-1, PEP, MacMARCKS, SNK, Stra13,  
7 kir/gem, EB12, IL1-R2, MyD116, RP105, uPAR, 4F2, hRab30, Id3, BKLf, LKLF, EFP,  
8 bcl-3, caspase 2, GILZ, hIFI-204, hRhoH, TRAF5, LT-beta, IFNg-RII, gadd45, CDC47,  
9 NAG, scd2, kappa 0 ig, iap38, G7e, B29, and SCD2.

1 16. A method of evaluating the effect of an immunosuppressive drug  
2 comprising:  
3 a) administering the drug to a patient;  
4 b) removing a cell sample from the patient; and  
5 c) determining the expression profile of the cell sample.

1 17. A method according to claim 16 further comprising comparing the  
2 expression profile to an expression profile of a healthy individual.

1 18. A method according to claim 16 wherein the expression profile  
2 includes at least one gene selected from the group consisting of Egr-1, Egr-2, Nur77, c-  
3 myc, MIP-1a, MIP-1b, BL34, gfi-1, NAB2, neurogranin, SLAP, A1, E2-20K, SATB1,  
4 Cctq, kappa V, pcp-4, TGIF, CD83, ApoE, Aeg-2, CD72, cyclin D2, lck, MEF-2C, bmk,  
5 IgD, Evi-2, vimentin, CD36, c-fes, c-fos, TRAP, hIP30, Ly6E.1, LRG-21, Fos B,  
6 gadd153, mafK, Ah-R, C/EBP beta, EZF, TIS7, TIS11, TIS11b, LSIRF, MKP1, PAC-1,  
7 PEP, MacMARCKS, SNK, Stra13, kir/gem, EB12, IL1-R2, MyD116, RP105, uPAR,  
8 4F2, hRab30, Id3, BKLf, LKLF, EFP, bcl-3, caspase 2, GILZ, hIFI-204, hRhoH,  
9 TRAF5, LT-beta, IFNg-RII, gadd45, CDC47, NAG, scd2, kappa 0 ig, iap38, G7e, B29,  
10 and SCD2.

1 19. An array of probes, comprising a support bearing a plurality of  
2 nucleic acid probes complementary to a plurality of mRNAs fewer than 1000 in number,  
3 wherein the plurality of mRNA probes includes an mRNA expressed by a gene selected  
4 from the group consisting of Egr-1, Egr-2, Nur77, c-myc, MIP-1a, MIP-1b, BL34, gfi-1,  
5 NAB2, neurogranin, SLAP, A1, E2-20K, SATB1, Cctq, kappa V, pcp-4, TGIF, CD83,  
6 ApoE, Aeg-2, CD72, cyclin D2, lck, MEF-2C, bmk, IgD, Evi-2, vimentin, CD36, c-fes,  
7 c-fos, TRAP, hIP30, Ly6E.1, LRG-21, Fos B, gadd153, mafK, Ah-R, C/EBP beta, EZF,  
8 TIS7, TIS11, TIS11b, LSIRF, MKP1, PAC-1, PEP, MacMARCKS, SNK, Stra13,  
9 kir/gem, EB12, IL1-R2, MyD116, RP105, uPAR, 4F2, hRab30, Id3, BKLf, LKLF, EFP,  
10 bcl-3, caspase 2, GILZ, hIFI-204, hRhoH, TRAF5, LT-beta, IFNg-RII, gadd45, CDC47,  
11 NAG, scd2, kappa 0 ig, iap38, G7e, B29, and SCD2.

1 20. The array of claim 19, wherein the probes are cDNA sequences.

1 21. The array of claim 19, comprising a plurality of sets of probes,  
2 each set of probes complementary to subsequences from a mRNA.